



02/18/97

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANT: Rodriguez, Moses  
Miller, David J.  
Asakura, Kunihiko

(ii) TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM REMYELINATION  
USING MONOCLONAL AUTOANTIBODIES

(iii) NUMBER OF SEQUENCES: 37

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: David A. Jackson, Esq.  
(B) STREET: 411 Hackensack Ave, Continental Plaza, 4th  
Floor  
(C) CITY: Hackensack  
(D) STATE: New Jersey  
(E) COUNTRY: USA  
(F) ZIP: 07601

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/692,084  
(B) FILING DATE: 08-AUG-1996  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/236,520  
(B) FILING DATE: 29-APR-1994

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Jackson Esq., David A.  
(B) REGISTRATION NUMBER: 26,742  
(C) REFERENCE/DOCKET NUMBER: 1199-1-001 CIP

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 201-487-5800  
(B) TELEFAX: 201-343-1684

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 420 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mus musculus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGGGATGGA GATGGATCTT TCTTTCCCTC CTGTCAGGAA CTGCAGGTGT CCATGCCAG	60
GTTCAAGCTGC AGCAGTCTGG ACCTGAGCTG GTGAAGCCTG GGGCTTAGT GAAGATATCC	120
TGCAAGGCTT CTGGTTACAC CTTCACAAAGC TACGATATAA ACTGGGTGAA GCAGAGGCCT	180
GGACAGGGAC TTGAGTGGAT TGGATGGATT TATCCTGGAG ATGGTAGTAC TAAGTACAAT	240
GAGAAATTCA AGGGCAAGGC CACACTGACT GCAGACAAAT CCTCCAGCAC AGCCTACATG	300
CAGCTCAGCA GCCTGACTTC TGAGAACTCT GCAGTCTATT TCTGTGCAAG AGGGGCCAGG	360
TTCTACTGGT ACTTCGATGT CTGGGGCGCA GGGACCACGG TCACCGTCTC CTCAGAGAGT	420

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 405 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mus musculus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGGCTGTCT TGGGGCTGCT CTTCTGCCTG GTGACATTCC CAAGCTGTGT CCTATCCCAG	60
GTGCAGCTGA AGCAGTCAGG ACCTGGCCTA GTGCAGCCCT CACAGAGCCT GTCCATCACC	120
TGCACAGTCT CTGGTTCTC ATTAACTAGC TATGGTGTAC ACTGGGTTCG CCAGTCTCCA	180

GGAAAGGGTC TGGAGTGGCT GGGAGTGATA TGGAGTGGTG GAAGCACAGA CTATAATGCA	240
GCTTTCATAT CCAGACTGAG CATCAGCAAG GACGCTTCCA AGAGCCAAGT TTTCTTTAAA	300
ATGAACAGTC TGCACCGCTAC TGACACAGCC ATATATTATT GTGCCAGAGA CTACGGTAGT	360
AGGGGGGACT ACTGGGTCA AGGAACCTCA GTCACCGTCT CCTCA	405

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 423 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *Mus musculus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGAAGTTGT GGTTAAACTG GGTTTTCTT TTAACACTTT TACATGGTAT CCAGTGTGAG	60
GTTGAAGCTGG TGGAAATCTGG TGGAGGCCTG GTACAGCCTG GGGGTTCTCT GAGACTCTCC	120
TGTGCAACTT CTGGGTTCAC CTTCAGTGAT TTCTACATGG AGTGGGTCCG CCAGCCTCCA	180
GGGAAGAGAC TGGAGTGGAT TGCTGCAAGT AGAAAGAAAG CTAATGATTA TAAAACAGAG	240
TACAGTGCAT CTGTGAAGGG CGGGTTCACCC GTCTCCAGAG ACACCTCCCA AAGCATCCTC	300
TACCTTCAGA TGAATGCCCT GAGAGATGAG GACACTGCCA TTTATTACTG TGCAAGAGAT	360
GCACGGCAGC TCGGGCTCCC GTTGCTTAC TGGGGCCAAG GGACTCTGGT CACTGTCTCT	420
GCA	423

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 384 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mus musculus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATGGAATCAC AGACTCTGGT CTTCATATCC ATACTGCTCT GGTTATATGG AGCTGATGGG	60
AACATTGTAA TGACCCAATC TCCCAAATCC ATGTCCATGT CAGTAGGAGA GAGGGTCACC	120
TTGACCTGCA AGGCCAGTGA GAATGTGGTT ACTTATGTTT CCTGGTATCA ACAGAAACCA	180
GAGCAGTCTC CTAAACTGCT GATATAACGGG GCATCCAACC GGTACACTGG GGTCCCCGAT	240
CGCTTCACAG GCAGTGGATC TGCAACAGAT TTCACTCTGA CCATCAGCAG TGTGCAGGCT	300
GAAGACCTTG CAGATTATCA CTGTGGACAG GGTTACAGCT ATCCGTACAC GTTCCGAGGG	360
GGGACCAAGC TGGAAATAAA ACGG	384

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mus musculus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGGACATGA GGGCTCCTGC ACAGATTTTT GGCTTCTTGT TGCTCTTGT TCAAGGTACC	60
AGATGTGACA TCCAGATGAC CCAGTCTCCA TCCTCCTTAT CTGCCTCTCT GGGAGAAAGA	120
GTCAGTCTCA CTTGTCGGGC AAGTCAGGAC ATTGGTAGTA GCTTAAACTG GCTTCAGCAG	180
GAACCAGATG GAACTATTAA ACGCCTGATC TACGCCACAT CCAGTTAGA TTCTGGTGTG	240
CCCAAAAGGT TCAGTGGCAG TAGGTCTGGG TCAGATTATT CTCTCACCAC CAGCAGCCTT	300
GAGTCTGAAG ATTTGTAGA CTATTACTGT CTACAATATG CTAGTTCTCC GTACACGTT	360

GGAGGGGGGA CCAAGCTGGA AATAAAACGG GCTGATGCTT CA

402

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 396 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *Mus musculus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATGGAGTCAC AGATTCAAGGT CTTTGTATTC GTGTTCTCT GGTTGTCTGG TGTTGACGGA	60
GACATTGTGA TGACCCAGTC TCACAAATTC ATGTCCACTT CAGTAGGAGA CAGGGTCAGC	120
ATCACCTGCA AGGCCAGTCA GGATGTGAGT ACTGCTGTAG CCTGGTATCA ACAGAAACCA	180
GGACAATCTC CTAAACTACT GATTTACTCG GCATCCTACC GGTACACTGG AGTCCCTGAT	240
CGCTTCACTG GCAGTGGATC TGGGACGGAT TTCACTTCA CCATCAGCAG TGTGCAGGCT	300
GAAGACCTGG CAGTTTATTA CTGTCAGCAA CATTATACTA CTCCGCTCAC GTTCGGTGCT	360
GGGACCAGGC TGGAGCTGAA ACGGGCTGAT GCTTCA	396

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 417 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *Mus musculus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATGGCTGTCT TGGGGCTGCT CTTCTGCCTG GTGACATTCC CAAGCTGTGT CCTATCCCAG	60
GTGCAGCTGA GGCAGTCAGG ACCTGGCCTA GTGCAGCCCT CACAGAGCCT GTCCATCACC	120
TGCACAGTCT CTGGTTCTC ATTAACTAGC TATGGTGTAC ACTGGTTTCG CCAGTCTCCA	180
GGAAAGGGTC TGGAGTGGCT GGGAGTGATA TGGAGTGGTG GAAGCACAGA CTATAATGCA	240
GCTTTCATAT CCAGACTGAG CATCAGCAAG GACAATTCCA AGAGCCAAGT TTTCTTTAAA	300
ATGAACAGTC TGCAAGCTAA TGACACAGCC ATATATTACT GTGCCAGAAA TAGGGTAGG	360
TACAATTACT ATGCTATGGA CTACTGGGGT CAAGGAACCT CAGTCACCGT CTCCTCA	417

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 384 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATGGAATCAC AGACTCTGGT CTTCATATCC ATACTGCTCT GGTTATATGG AGCTGATGGG	60
AACATTGTAA TGACCCAATC TCCCAAATCC ATGTCCATGT CAGTAGGAGA GAGGGTCACC	120
TTGACCTGCA AGGCCAGTGA GAATGTGGTT ACTTATGTTT CNTGGTATCA ACAGAACCA	180
GAGCAGTCCTC CTAAACTGCT GATATATGGG GCATCCAACC GGTACACTGG GGTCCNGAT	240
CGCTTCACAG GCAGTGGATC TGCAACAGAT TTCACTCTGA CCATCAGCAG TGTGCAGGCT	300
GAAGACCTTG CAGATTATCA CTGTGGACAG GGTTACAGCT ATCCGTACAC GTTCCGAGGG	360
GGGACCAAGC TGGAAATAAA ACGG	384

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 351 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGGGATGGA GATGGATCTT TCTTTCCCTC CTGTCAGGAA CTGCAGGTGT CCATTGCCAG	60
GTTCAAGCTGC AGCAGTCTGG ACCTGAGCTG GTGAAGCCTG GGGCTTAGT GAAGATATCC	120
TGCAAGGCTT CTGGTTACAC CTTCACAAAGC TACGATATAA ACTGGGTGAA GCAGAGGCCT	180
GGACAGGGAC TTGAGTGGAT TGGATGGATT TATCCTGGAG ATGGTAGTAC TAAGTACAAT	240
GAGAAATTCA AGGGCAAGGC CACACTGACT GCAGACAAAT CCTCCAGCAC AGCCTACATG	300
CAGCTCAGCA GCCTGACTTC TGAGAACTCT GCAGTCTATT TCTGTGCAAG A	351

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TACTGGTACT TCGATGTCTG GGGCGCAGGG ACCACGGTCA CCGTTCCCTC AGAGAGT	57
--	----

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 348 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATGGCTGTCT TGGGGCTGCT CTTCTGCCTG GTGACATTCC CAAGCGGTGT CCTATCCCAG	60
GTGCAGCTGA AGCAGTCAGG ACCTGGCCTA GTGCAGCCCTCACAGAGCCT GTCCATCACC	120
TGCACAGTCT CTGGTTTCTC ATTAACTAGC TATGGTGTAC ACTGGGTTCG CCAGTCTCCA	180
GGAAAGGGTC TGGAGTGGCT GGGAGTGATA TGGAGTGGTG GAAGCACAGA CTATAATGCA	240
GCTTTCATAT CCAGACTGAG CATCAGCAAG GACAATTCCA AGAGCCAAGT TTTCTTTAAA	300
ATGAACAGTC TGCAAGCTAA TGACACAGCC ATATATTACT GTGCCAGA	348

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATGGCTGTCT TAGGGCTGCT CTTCTGCCTA GTGACATTCC CAAGCGGTGT CCTATCCCAG	60
GTGCAGCTGA AGCAGTCAGG ACCTGGCCTA GTGCAGCCCTCACAGAGCCT GTCCATCACC	120
TGCACAGTCT CTGGTTTCTC ATTAACTAGC TATGGTGTAC ACTGGGTTCG CCAGTCTCCA	180
GGAAAGGGTC TGGAGTGGCT GGGAGTGATA TGGAGTGGTG GAAGCACAGA CTATAATGCA	240
GCTTTCATAT CCAGACTGAG CATCAGCAAG GACAATTCCA AGAGCCAAGT TTTCTTTAAA	300
ATGAACAGTC TGCAATCTAA TGACACAGCC ATATATTACT GTGCCAGA	348

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TACTATGCTA TGGACTACTG GGGTCAAGGA ACCTCAGTCA CCGTCTCCTC A

51

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATGAAGTTGT GGTTAAACTG GGTTCCTT TTAACACTTT TACATGGTAT CCAGTGTGAG 60  
GTGAAGCTGG TGGAATCTGG AGGAGGCTTG GTACAGCCTG GGGGTTCTCT GAGACTCTCC 120  
TGTGCAACTT CTGGGTTCAC CTTCACTGAT TTCTACATGG AGTGGGTCCG CCAGCCTCCA 180  
GGGAAGAGAC TGGAGTGGAT TGCTGCAAGT AGAAACAAAG CTAATGATTA TACAACAGAG 240  
TACAGTGCAT CTGTGAAGGG TCGGTTCATC GTCTCCAGAG ACACTTCCA AAGCATCCTC 300  
TACCTTCAGA TGAATGCCCT GAGAGCTGAG GACACTGCCA TTTATTACTG TGCAAGAGAT 360  
GCAC 364

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCCTGGTTTG CTTACTGGGG CCAAGGGACT CTGGTCAGT TCTCTGCA

48

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ATGGACATGA GGGCTCCTGC ACAGATTGTT GGCTTCTTGT TGCTCTGTT TCAAGGTACC

60

AGATGTGACA TCCAGATGAC CCAGTCTCCA TCCTCCTTAT CTGCCTCTCT GGGAGAAAGA

120

GTCAGTCTCA CTTGTCGGGC AAGTCAGGAC ATTGGTAGTA GCTTAAACTG GCTTCAGCAG

180

GAACCAGATG GAACTATTAA ACGCCTGATC TACGCCACAT CCAGTTAGA TTCTGGTGTG

240

CCCAAAGGT TCAGTGGCAG TAGGTCTGGG TCAGATTATT CTCTCACCAT CAGCAGCCTT

300

GAGTCTGAAG ATTTGTAGA CTATTACTGT CTACAATATG CTAGTTCTCC G

351

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATGGACATGA GGGCTCCTGC ACAGATTGTT GGCTTCTTGT TGCTCTGTT TCAAGGTACC

60

AGATGTGACA TCCAGATGAC CCAGTCTCCA TCCTCCTTAT CTGCCTCTCT GGGAGAAAGA

120

GTCAGTCTCA CTTGTCGGGC AAGTCAGGAC ATTGGTAGTA GCTTAAACTG GCTTCAGCAG 180  
GAACCAGATG GAACTATTAA ACGCCTGATC TACGCCACAT CCAGTTAGA TTCTGGTGTC 240  
CCCAAAAGGT TCAGTGGCAG TAGGTCTGGG TCAGATTATT CTCTCACCAT CAGCAGCCTT 300  
GAGTCTGAAG ATTTTGTAGA CTATTACTGT CTACAATATG CTAGTTCTCC T 351

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TACACGTTCG GAGGGGGGAC CAAGCTGGAA ATAAAACGGG CTGATGCTTC A 51

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CTCACGTTCG GTGCTGGGAC CAAGCTGGAG CTGAAACGGG CTGATGCTTC A 51

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 393 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 1..393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATG ATG TCC TCT GCT CAG TTC CTT GGT CTC CTG TTG CTC TGT TTT CAA 48  
Met Met Ser Ser Ala Gln Phe Leu Gly Leu Leu Leu Cys Phe Gln  
1 5 10 15

GGT ACC AGA TGT GAT ATC CAG ATG ACA CAG ACT ACA TCC TCC CTG TCT 96  
Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Thr Ser Ser Leu Ser  
20 25 30

GCC TCT CTG GGA GAC AGA GTC ACC ATC AGT TGC AGG GCA AGT CAG GAC 144  
Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp  
35 40 45

ATT AGC AAT TAT TTA AAC TGG TAT CAG CAG AAA CCA GAT GGA ACT GTT 192  
Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val  
50 55 60

AAA CTC CTG ATC TAC TAC ACA TCA AGA TTA CAC TCA GGA GTC CCA TCA 240  
Lys Leu Leu Ile Tyr Tyr Ser Arg Leu His Ser Gly Val Pro Ser  
65 70 75 80

AGG TTC AGT GGC AGT GGG TCT GGA ACA GAT TAT TCT CTC ACC ATT AGC 288  
Arg Phe Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser  
85 90 95

AAC CTG GAG CAA GAA GAT ATT GCC ACT TAC TTT TGC CAA CAG GGT AAT 336  
Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Asn  
100 105 110

ACG CTT CCG TGG ACG TTC GGT GGA GGC ACC AAG CTG GAA ATC AAA CGG 384  
Thr Leu Pro Trp Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys Arg  
115 120 125

GCT GAT GCT 393

Ala Asp Ala  
130

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 131 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Met Ser Ser Ala Gln Phe Leu Gly Leu Leu Leu Cys Phe Gln  
1 5 10 15

Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser  
20 25 30

Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp  
35 40 45

Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val  
50 55 60

Lys Leu Leu Ile Tyr Tyr Ser Arg Leu His Ser Gly Val Pro Ser  
65 70 75 80

Arg Phe Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser  
85 90 95

Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn  
100 105 110

Thr Leu Pro Trp Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys Arg  
115 120 125

Ala Asp Ala  
130

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GATATCCAGA TGACACAGAC TACATCCTCC CTGTCGCCT CTCTGGGAGA CAGAGTCACC	60
ATCAGTTGCA GGGCAAGTCA GGACATTAGC AATTATTTAA ACTGGTATCA GCAGAAACCA	120
GATGGAACTG TTAAACTCCT GATCTACTAC ACATCAAGAT TACACTCAGG AGTCCCATCA	180
AGGTTCAGTG GCAGTGGTC TGGAACAGAT TATTCTCTCA CCATTAGCAA CCTGGAGCAA	240
GAAGATATTG CCACTTACTT TTGCCAACAG GGTAATAACGC TTCCTCCGAC GTTCGGTGGA	300
GGCACCAAGC TGGAAATCAA ACGG	324

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GATATCCAGA TGACACAGAC TACATCCTCC CTGTCGCCT CTCTGGGAGA CAGAGTCACC	60
ATCAGTTGCA GGGCAAGTCA GGACATTAGC AATTATTTAA ACTGGTATCA GCAGAAACCA	120
GATGGAACTG TTAAACTCCT GATCTACTAC ACATCAAGAT TACACTCAGG AGTCCCATCA	180

AGGTTCAGTG GCAGTGGTC TGGAACAGAT TATTCTCTCA CCATTAGCAA CCTGGAGCAA 240

GAAGATATTG CCACTTACTT TTGCCAACAG GGTAATACGC TTCCT 285

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TGGACGTTCG GTGGAGGCAC CAAGCTGGAA ATCAAACGT 39

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 429 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..429

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ATG GGA TGG AGC TGT ATC ATC CTC TTT TTG GTA GCA GCA GCT ACA GGT  
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Ala Ala Thr Gly 48  
1 5 10 15

GTC CAC TCC CAG GTC CAA CTG CAG CAG CCT GGG ACT GAA CTG GTG AAG  
Val His Ser Gln Val Gln Leu Gln Gln Pro Gly Thr Glu Leu Val Lys 96  
20 25 30

CCT GGG GCT TCA GTG AAG CTG TCC TGC AAG GCT TCT GGC TAC ACC TTC 144

Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe			
35	40	45	
ACC AGC TAC TGG ATG CAC TGG GTG AAG CAG AGG CCT GGA CAA GGC CTT			192
Thr Ser Tyr Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu			
50	55	60	
GAG TGG ATT GGA AAT ATT AAT CCT AGC AAT GGT GGT ACT AAC TAC AAT			240
Glu Trp Ile Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn			
65	70	75	80
GAG AAG TTC AAG AGC AAG GCC ACA CTG ACT GTA GAC AAA TCC TCC AGC			288
Glu Lys Phe Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser			
85	90	95	
ACA GCC TAC ATG CAG CTC AGC AGC CTG ACA TCT GAG GAC TCT GCG GTC			336
Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val			
100	105	110	
TAT TAT TAT GCA AGA CGG GCC CCT TAC TAC GGT AGT AGG AAC TTT GAC			384
Tyr Tyr Tyr Ala Arg Arg Ala Pro Tyr Tyr Gly Ser Arg Asn Phe Asp			
115	120	125	
TAC TGG GGC CAA GGC ACC ACT CTC ACA GTC TCC TCA GAG AGT CAG			429
Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Glu Ser Gln			
130	135	140	

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:

  - (A) LENGTH: 143 amino acids
  - (B) TYPE: amino acid
  - (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Ala Ala Thr Gly  
 1 5 10 15

Val His Ser Gln Val Gln Leu Gln Gln Pro Gly Thr Glu Leu Val Lys  
20 25 30

Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
35 40 45

Thr Ser Tyr Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu  
50 55 60

Glu Trp Ile Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn  
65 70 75 80

Glu Lys Phe Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser  
85 90 95

Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val  
100 105 110

Tyr Tyr Tyr Ala Arg Arg Ala Pro Tyr Tyr Gly Ser Arg Asn Phe Asp  
115 120 125

Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Glu Ser Gln  
130 135 140

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CAG GTC CAA CTG CAG CAG CCT GGG ACT GAA CTG GTG AAG CCT GGG GCT  
Gln Val Gln Leu Gln Gln Pro Gly Thr Glu Leu Val Lys Pro Gly Ala  
1 5 10 15

TCA GTG AAG CTG TCC TGC AAG GCT TCT GGC TAC ACC TTC ACC AGC TAC Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr	96
20 25 30	
 TGG ATG CAC TGG GTG AAG CAG AGG CCT GGA CAA GGC CTT GAG TGG ATT Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile	144
35 40 45	
 GGA AAT ATT AAT CCT AGC AAT GGT GGT ACT AAC TAC AAT GAG AAG TTC Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn Glu Lys Phe	192
50 55 60	
 AAG AGC AAG GCC ACA CTG ACT GTA GAC AAA TCC TCC AGC ACA GCC TAC Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr	240
65 70 75 80	
 ATG CAG CTC AGC AGC CTG ACA TCT GAG GAC TCT GCG GTC TAT TAT TAT Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Tyr	288
85 90 95	
 GCA AGA GAT TAC TAC GGT AGT AGC TGG GGG TAC TAC TTT GAC TAC TGG Ala Arg Asp Tyr Tyr Gly Ser Ser Trp Gly Tyr Tyr Phe Asp Tyr Trp	336
100 105 110	
 GGC CAA GGC ACC ACT CTC ACA GTC TCC TCA Gly Gln Gly Thr Thr Leu Thr Val Ser Ser	366
115 120	

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 122 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Gln Val Gln Leu Gln Gln Pro Gly Thr Glu Leu Val Lys Pro Gly Ala  
1 5 10 15

DRAFT DRAFT DRAFT

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
20 25 30

Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile  
35 40 45

Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn Glu Lys Phe  
50 55 60

Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr  
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Tyr  
85 90 95

Ala Arg Asp Tyr Tyr Gly Ser Ser Trp Gly Tyr Tyr Phe Asp Tyr Trp  
100 105 110

Gly Gln Gly Thr Thr Leu Thr Val Ser Ser  
115 120

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ATGGGATGGA GCTGTATCAT CCTCTTTTG GTAGCAGCAG CTACAGGTGT CCACTCCCAG 60

GTCCAAGTGC AGCAGCCTGG GACTGAAGTG GTGAAGCCTG GGGCTTCAGT GAAGCTGTCC 120

TGCAAGGCTT CTGGCTACAC CTTCACCCAGC TACTGGATGC ACTGGGTGAA GCAGAGGCCT 180

GGACAAGGCC TTGAGTGGAT TGGAAATATT AATCCTAGCA ATGGTGGTAC TAACTACAAT 240

GAGAAGTTCA AGAGCAAGGC CACACTGACT GTAGACAAAT CCTCCAGCAC AGCCTACATG 300

CAGCTCAGCA GCCTGACATC TGAGGACTCT GCGGTCTATT ATTATGCAAG A 351

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TACTTGACT ACTGGGGCCA AGGCACCCT CTCACAGTCT CCTCA 45

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mus musculus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Met Gly Trp Arg Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly  
1 5 10 15

Val His Cys Gln Val Gln Leu Gln Ser Gly Pro Glu Leu Val Lys  
20 25 30

Pro Gly Ala Leu Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
35 40 45

Thr Ser Tyr Asp Ile Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu  
50 55 60

Glu Trp Ile Gly Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys Tyr Asn  
 65 70 75 80  
 Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser  
 85 90 95  
 Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asn Ser Ala Val  
 100 105 110  
 Tyr Phe Cys Ala Arg Gly Ala Arg Phe Tyr Trp Tyr Phe Asp Val Trp  
 115 120 125  
 Gly Ala Gly Thr Thr Val Thr Val Ser Ser  
 130 135

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 135 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *Mus musculus*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Ala Val Leu Gly Leu Leu Phe Cys Leu Val Thr Phe Pro Ser Cys  
 1 5 10 15  
 Val Leu Ser Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln  
 20 25 30  
 Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu  
 35 40 45  
 Thr Ser Tyr Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu  
 50 55 60  
 Glu Trp Leu Gly Val Ile Trp Ser Gly Gly Ser Thr Asp Tyr Asn Ala  
 65 70 75 80  
 Ala Phe Ile Ser Arg Leu Ser Ile Ser Lys Asp Ala Ser Lys Ser Gln  
 85 90 95

DRAFT Sequence Database

Val Phe Phe Lys Met Asn Ser Leu His Ala Thr Asp Thr Ala Ile Tyr  
100 105 110

Tyr Cys Ala Arg Asp Tyr Gly Ser Arg Gly Asp Tyr Trp Gly Gln Gly  
115 120 125

Thr Ser Val Thr Val Ser Ser  
130 135

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mus musculus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Met Lys Leu Trp Leu Asn Trp Val Phe Leu Leu Thr Leu Leu His Gly  
1 5 10 15

Ile Gln Cys Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Gln  
20 25 30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe  
35 40 45

Ser Asp Phe Tyr Met Glu Trp Val Arg Gln Pro Pro Gly Lys Arg Leu  
50 55 60

Glu Trp Ile Ala Ala Ser Arg Lys Lys Ala Asn Asp Tyr Lys Thr Glu  
65 70 75 80

Tyr Ser Ala Ser Val Lys Gly Arg Phe Thr Val Ser Arg Asp Thr Ser  
85 90 95

Gln Ser Ile Leu Tyr Leu Gln Met Asn Ala Leu Arg Asp Glu Asp Thr  
100 105 110

Ala Ile Tyr Tyr Cys Ala Arg Asp Ala Arg Gln Leu Gly Leu Pro Phe  
115 120 125

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala  
130 135 140

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 128 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *Mus musculus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Glu Ser Gln Thr Leu Val Phe Ile Ser Ile Leu Leu Trp Leu Tyr  
1 5 10 15

Gly Ala Asp Gly Asn Ile Val Met Thr Gln Ser Pro Lys Ser Met Ser  
20 25 30

Met Ser Val Gly Glu Arg Val Thr Leu Thr Cys Lys Ala Ser Glu Asn  
35 40 45

Val Val Thr Tyr Val Ser Trp Tyr Gln Gln Lys Pro Glu Gln Ser Pro  
50 55 60

Lys Leu Leu Ile Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp  
65 70 75 80

Arg Phe Thr Gly Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr Ile Ser  
85 90 95

Ser Val Gln Ala Glu Asp Leu Ala Asp Tyr His Cys Gly Gln Gly Tyr  
100 105 110

Ser Tyr Pro Tyr Thr Phe Arg Gly Gly Thr Lys Leu Glu Ile Lys Arg  
115 120 125

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 130 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mus musculus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Met Asp Met Arg Ala Pro Ala Gln Ile Phe Gly Phe Leu Leu Leu  
1 5 10 15

Phe Gln Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser  
20 25 30

Leu Ser Ala Ser Leu Gly Glu Arg Val Ser Leu Thr Cys Arg Ala Ser  
35 40 45

Gln Asp Ile Gly Ser Ser Leu Asn Trp Leu Gln Gln Glu Pro Asp Gly  
50 55 60

Thr Ile Lys Arg Leu Ile Tyr Ala Thr Ser Ser Leu Asp Ser Gly Val  
65 70 75 80

Pro Lys Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr  
85 90 95

Ile Ser Ser Leu Glu Ser Glu Asp Phe Val Asp Tyr Tyr Cys Leu Gln  
100 105 110

Tyr Ala Ser Ser Pro Tyr Thr Phe Gly Gly Thr Lys Leu Glu Ile  
115 120 125

Lys Arg  
130

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 128 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mus musculus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met Glu Ser Gln Ile Gln Val Phe Val Phe Val Phe Leu Trp Leu Ser  
1 5 10 15

Gly Val Asp Gly Asp Ile Val Met Thr Gln Ser His Lys Phe Met Ser  
20 25 30

Thr Ser Val Gly Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asp  
35 40 45

Val Ser Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro  
50 55 60

Lys Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Thr Gly Val Pro Asp  
65 70 75 80

Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser  
85 90 95

Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln His Tyr  
100 105 110

Thr Thr Pro Leu Thr Phe Gly Ala Gly Thr Arg Leu Glu Leu Lys Arg  
115 120 125

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mus musculus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Met Ala Val Leu Gly Leu Leu Phe Cys Leu Val Thr Phe Pro Ser Cys  
1 5 10 15

Val Leu Ser Gln Val Gln Leu Arg Gln Ser Gly Pro Gly Leu Val Gln  
20 25 30

Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu  
35 40 45

Thr Ser Tyr Gly Val His Trp Phe Arg Gln Ser Pro Gly Lys Gly Leu  
50 55 60

Glu Trp Leu Gly Val Ile Trp Ser Gly Gly Ser Thr Asp Tyr Asn Ala  
65 70 75 80

Ala Phe Ile Ser Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln  
85 90 95

Val Phe Phe Lys Met Asn Ser Leu Gln Ala Asn Asp Thr Ala Ile Tyr  
100 105 110

Tyr Cys Ala Arg Asn Arg Gly Arg Tyr Asn Tyr Tyr Ala Met Asp Tyr  
115 120 125

Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser  
130 135